Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

	EXAMINER

ART UNIT	PAPER NUMBER
	9

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application.

Commissioner of Patents

Serial No. 09/312,596

1.   The reply filed 3 November 2000 (Paper No. 9) is not fully responsive to the communication mailed 28 May 1999 (Paper No. 3) for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules or CRF Diskette Problem Report.

Since the above-mentioned reply appears to be *bona fide*, applicant is given a TIME PERIOD of **ONE (1) MONTH** or **THIRTY (30) DAYS**, from the mailing date of this notice, whichever is longer, within which to supply the omission or correction in order to avoid abandonment. EXTENSIONS OF THIS TIME LIMIT MAY BE GRANTED UNDER 37 CFR 1.136(a).

2.   Any inquiry concerning this communication or earlier communications from the examiner should be directed to Michael Pak, whose telephone number is (703) 305-7038. The examiner can normally be reached on Monday through Friday from 5:50 AM to 2:20 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Yvonne Eyler, can be reached on (703) 308-6564.

Official papers filed by fax should be directed to (703) 308-4242. Faxed draft or informal communications with the examiner should be directed to (703) 308-0294.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Michael D. Pak
Michael Pak
Primary Patent Examiner
Art Unit 1646
18 December 2000

Application No.: 09/312,596

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other:

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: _O9/3l2, 596_

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TECH CENTER 1600/2900

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid
Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ✓ Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism
(NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature
(NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

M. Rik

1646

```
        RAW SEQUENCE LISTING                DATE: 11/20/2000
        PATENT APPLICATION:  US/09/312,596    TIME: 08:38:37

           Input Set : A:\593601.app
           Output Set: N:\CRF3\11202000\I312596.raw
```

```
 3  <110> APPLICANT: Rolo, Lorna W.
 4          Talmage, David
 5          Bao, Jianxin
 7  <120> TITLE OF INVENTION: A-FORM OF CYTOPLASMIC DOMAIN OF NARIA (CRD-NEUREGULIN
 8          AND USES THEREOF
10  <130> FILE REFERENCE: 0575/59360
12  <140> CURRENT APPLICATION NUMBER: 09/312,596
13  <141> CURRENT FILING DATE: 1999-05-14
15  <160> NUMBER OF SEQ ID NOS: 4
17  <170> SOFTWARE: PatentIn Ver. 2.1
19  <210> SEQ ID NO: 1
20  <211> LENGTH: 3212
21  <212> TYPE: DNA
22  <213> ORGANISM: CHICKEN NARIA
24  <400> SEQUENCE: 1
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26  ctccttctac cgcatgacaa ttgtttttcct cgcctaagca gataccaacc tcagatgctc  120
27  aaggtgagag tcttgccttt cgctctgggc tatttggttca cttaatccgg tcaatttgtt  180
28  cgctgctcgt ggttgtcttt ctccccgccc tccttccccc tgttttgttt tgtttccgctt  240
29  gcttctcgggg agacggctcct tccctccagtc aggaagagctg gaattgcttg agaggcgtat 300
30  aaggaattat aaaagtggcc aggaaacacg agcgcagtga ctgcaggacct accctcggct  360
31  tcggcaaggac agcttgagcg acaaggggct cggcgcaggg gcgcgggggtc tccttttttcc 420
32  cgtgcgtttcc tcttctccca gttcggatga tgttgctgtt tcggacctct cgctgactcc  480
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34  acagtgatgg actgtgatag agttaaggcc tttttggaggt gagctgtgtc acagctgatg 600
35  cttaaacatg tctgaagtag gcaccgagac tttccccagc ccctcggctc agctgagccc 660
36  tgatgcatcc ctcggcgggc tccgggctga ggagaacatg cgggggcccc acagagaqga 720
37  caqcagggtc ccagttgtgg caggcctggc ctcgacctgc tgcgtgtgcc tqgaagcaga 780
38  tcgactgaag gactgcctca actctgagaa gatctgcatc gccctatcc tagcttgcct  840
39  actcagcctc tccctgca ttgctggcct caagtgggtc tttatgqaca agattttttga 900
40  gtatgactct cctacacacc ttgacctgg gaggataqga caaqacccaa qqaqcactgt  960
41  ggatcctaca gctctgtctg cctgggtgcc ttcggaggtg tatgcctcac cctcccat  1020
42  acctagcctt gagagcaagg ctgaagtgac agtgcaaact gacaactcgc tcgtgccctc 1080
43  caggcccttc cttcagcctt ctctctacaa ccgcatccta gatatcgggt tgtggtcctc 1140
44  tgccacaccg tcactgtcac catcctcccr ggagcctacc acggcatctc aggcacaagc 1200
45  aacagaaccc aatctccaaa ctgctccaaa acttccact tctacatcta caactggqac 1260
46  aagtcatctc acaaaatatg acataaagca gaaagccttc tgtgtaaatg gggaqaqtg  1320
47  ctacatggta aaaqacctcc caaaccctcc acgataccta tgcaggtacc caaatgaatt 1380
48  tactgqtgat cactgccaaa actacgtaat ggccagcttc tacaagcatc ttggqattqa 1410
49  atttatggaa gctgaggaac tgtaccagaa acgggtgctg accataactg gcattgcat  1500
50  tgctcttcta gtagttggca tcatgtatat ggtggctac tgcaaaacca agaagcagag 1560
51  gaaaaagttg catgaccgcc ttcggaagag ccttcgctca gagagqaaca acgttatgaa 1620
52  catggcaaat gggcacacc acrccaaccc accaccagac gatgtccagc tggtgaatca 1680
53  gtacgrttca aaaaacataa tctccagtga acgtgtcgtt gagcgagaaa ccagacctc  1740
54  gttttcccaca agccactaca cctcaacaac tcatcactcc atgacagtca cccagacgcc 1800
55  taqccacagc tggagtaatg gccataccga aaqcattctc tccgaaagcc actccgtgct 1860
56  cgtcagctcc tcagtgqaga atagcaggca caccagccca acagggccac gaggccgcct 1920
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RAW SEQUENCE LISTING   DATE: 11/20/2000
PATENT APPLICATION: US/09/312,596   TIME: 08:38:37

Input Set : A:\593601.app
Output Set: N:\CRF3\11202000\I312596.raw

```
57 caatggcatt ggtgggccaa gggaaggcaa cggcatgcaa gagagacccc 1980
58 tgactcctac cgagactctc ctcacagtga aaggtatgtc tcagctatga ccacaccagc 2040
59 tcgcatgtca cccgttgatt tccacactcc aacttctccc aagtcccctc catctgaaat 2100
60 gtcaccacca gtttccaget tgaccatctc catccettcg gtggcggtga gtcccttat 2160
61 ggacgaggag agaccgctgc tattggtgac cccaccacgg ctgcgtgaga agtacgacaa 2220
62 ccacctteag caattcaact cettecacaa caatcccacc catgagagca acagtctgcc 2280
63 accagtcct ctgaggatag tggaggatgu agagtatgag accacgcagg agtacgaacc 2340
64 agcacaggag cctccaaaga aactcaccaa cagccggagg gtgaaaagaa caaagcccaa 2400
65 tggccatatt tccagcaggg tagaagtgga ctccgacaca agtctcaga gcactagctc 2460
66 tgaagagcaa acagaagatg aaagaatagg tgaggataca ccattictta gcatacaaaa 2520
67 tcccatggca accagtctgg agccagcege tgcatatcgg ctggctgaga acaggactaa 2580
68 cccugcaaat cgcttctcca caccagaaga gttgcaagca aggttgtcca gtgtaatagc 2640
69 taaccaagac cctattgctg tataagacat aaacaaaac catagattca catgtaaaac 2700
70 tttatrttat ataatgaagt attccacctt taaattaaac aattattt attrtagcaa 2760
71 ttccgctgat agaaaacaag agtggaaaaa gaaactttta taaattaagt atacgtatgt 2820
72 acaaatgtgt tatgtgccat atgtagcaat tttttacagt atttccaaaa tgggggaaga 2880
73 tatcaatggt gcctttatgt tatgttatgt tgaagagcaag ttttgtacag ctacaatgat 2940
74 tgctgtcccg tagtatttg caaaacctic tagccctcag ttgttctggc tttttattgc 3000
75 attgcatrut aatgactgga rgtatgattt gcaaaaattg cagaagtccc catttgcttg 3060
76 ttgtgggaatc cccagatcaa aaagcctat tatggcactc acacectatc cacttcacca 3120
77 ggaaaaaaaa aaaatcaaaa aaaaaaaaa aaaaaaaga aaagaaagag aaaaaagaaa 3180
78 agaaaaagaa aaaaaaagct gaaaaaataa aa 3212
```

```
81 <210> SEQ ID NO: 2
82 <211> LENGTH: 1070
83 <212> TYPE: PRT
84 <213> ORGANISM: CHICKEN BARIA
86 <400> SEQUENCE: 2
87 Gly Cys Cys Cys Tyr Cys His Phe Cys Arg Cys Arg Cys Cys Tyr Arg
88  1                5                   10                  15
W--> 90 Phe Cys Phe Cys Ser Phe Tyr Arg Met Thr Ile Val Phe Leu Ala (Xaa)
     91              20                  25                  30
W--> 93 Ala Asp Thr Ser Leu Arg Cys Ser Arg (Xaa) Glu Ser Cys Leu Ser Leu
     94              35                  10                  45
96 Trp Ala Ile Gly Ser Leu Asn Pro Val Asn Leu Phe Ala Ala Arg Gly
97              50                  55                  60
99 Cys Leu Ser Pro Arg Pro Pro Ser Pro Cys Phe Val Leu Phe Arg Leu
100 65                 70                  75                  80
102 Leu Ser Gly Gly Arg Ser Phe Pro Gln Ser Glu Glu Leu Glu Leu Leu
103             85                  90                  95
105 Glu Arg Arg Ile Arg Asn Tyr Lys Ser Gly Gln Glu Thr Arg Ala Gln
106             100                 105                 110
W--> 108 (Xaa) Leu Gln Ser Cys Pro Trp Leu Arg Gln Gly Ser Val Ser Gly Arg
     109             115                 120                 125
111 Gly Leu Gly Gln Gly Ala Gly Gly Leu Leu Phe Pro Val Arg Ser Ser
112             130                 135                 140
114 Ser Pro Ser Ser Asp Asp Val Ala Val Ser Asp Leu Ser Leu Thr Pro
115 115                150                 155                 160
W--> 117 Ala Leu (Xaa) Phe Leu Leu Ser Ala Val Thr Val Thr Pro Ser Leu Ser
     118             165                 170                 175
```

[Handwritten annotation:] Missing mandatory <220> to <223> features to explain "Xaa's" in the sequence. See #10 on the Error Summary Sheet.

```
RAW SEQUENCE LISTING                     DATE: 11/20/2000
PATENT APPLICATION:  US/09/312,596       TIME: 08:38:37

Input Set : A:\593601.app
Output Set: N:\CRF3\11202000\I312596.raw
```

refer to p. 2

```
W--> 120 Val Cys Val Ser Gln Xaa Trp Thr Val Ile Glu Leu Arg Pro Phe Gly
     121                 180                 185                 190
W--> 123 Gly Glu Leu Cys His Ser Xaa Cys Leu Asn Met Ser Glu Val Gly Thr
     124             195                 200                 205
     126 Glu Thr Phe Pro Ser Pro Ser Ala Gln Leu Ser Pro Asp Ala Ser Leu
     127         210                 215                 220
     129 Gly Gly Leu Pro Ala Glu Glu Asn Met Pro Gly Pro His Arg Glu Asp
     130 225                 230                 235                 240
     132 Ser Arg Val Pro Gly Val Ala Gly Leu Ala Ser Thr Cys Cys Val Cys
     133             245                 250                 255
     135 Leu Glu Ala Glu Arg Leu Lys Gly Cys Leu Asn Ser Glu Lys Ile Cys
     136             260                 265                 270
     138 Ile Ala Pro Ile Leu Ala Cys Leu Leu Ser Leu Cys Leu Cys Ile Ala
     139         275                 280                 285
     141 Gly Leu Lys Trp Val Phe Val Asp Lys Ile Phe Glu Tyr Asp Ser Pro
     142         290                 295                 300
     144 Thr His Leu Asp Pro Gly Arg Ile Gly Gln Asp Pro Arg Ser Thr Val
     145 305                 310                 315                 320
     147 Asp Pro Thr Ala Leu Ser Ala Trp Val Pro Ser Glu Val Tyr Ala Ser
     148             325                 330                 335
     150 Pro Phe Pro Ile Pro Ser Leu Glu Ser Lys Ala Glu Val Thr Val Gln
     151         340                 345                 350
     153 Thr Asp Ser Ser Leu Val Pro Ser Arg Pro Phe Leu Gln Pro Ser Leu
     154         355                 360                 365
     156 Tyr Asn Arg Ile Leu Asp Val Gly Leu Trp Ser Ser Ala Thr Pro Ser
     157         370                 375                 380
     159 Leu Ser Pro Ser Ser Leu Glu Pro Thr Thr Ala Ser Glu Ala Gln Ala
     160 385                 390                 395                 400
     162 Thr Glu Thr Asn Leu Gln Thr Ala Pro Lys Leu Ser Thr Ser Thr Ser
     163             405                 410                 415
     165 Thr Thr Gly Thr Ser His Leu Thr Lys Cys Asp Ile Lys Gln Lys Ala
     166         420                 425                 430
     168 Phe Cys Val Asn Gly Gly Glu Cys Tyr Met Val Lys Asp Leu Pro Asn
     169         435                 440                 445
     171 Pro Pro Arg Tyr Leu Cys Arg Cys Pro Asn Glu Phe Thr Gly Asp Arg
     172         450                 455                 460
     174 Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu
     175 465                 470                 475                 480
     177 Phe Met Glu Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr
     178             485                 490                 495
     180 Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val Ala
     181         500                 505                 510
     183 Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg
     184         515                 520                 525
     186 Gln Ser Leu Arg Ser Glu Arg Asn Asn Val Met Asn Met Ala Asn Gln
     187     530                 535                 540
     189 Pro His His Pro Asn Pro Pro Asp Asn Val Gln Leu Val Asn Gln
     190 545                 550                 555                 560
     192 Tyr Val Ser Lys Asn Ile Ile Ser Ser Glu Arg Val Val Glu Arg Glu
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RAW SEQUENCE LISTING   DATE: 11/20/2000
PATENT APPLICATION: US/09/312,596   TIME: 08:38:37

Input Set : A:\593601.app
Output Set: N:\CRF3\11202000\I312596.raw

```
193                565                570                575
195 Thr Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Thr His His
196           580                585                590
198 Ser Met Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly His
199           595                600                605
201 Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Leu Val Ser Ser Ser
202      610                615                620
204 Val Glu Asn Ser Arg His Thr Ser Pro Thr Gly Pro Arg Gly Arg Leu
205 625           630                635                640
207 Asn Gly Ile Gly Gly Pro Arg Glu Gly Asn Ser Phe Leu Arg His Ala
208           645                650                655
210 Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser Glu Arg Tyr
211           660                665                670
213 Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro Val Asp Phe His
214           675                680                685
216 Thr Pro Thr Ser Pro Lys Ser Pro Pro Ser Glu Met Ser Pro Pro Val
217      690                695                700
219 Ser Ser Leu Thr Ile Ser Ile Pro Ser Val Ala Val Ser Pro Phe Met
220 705           710                715                720
222 Asp Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu Arg Glu
223           725                730                735
225 Lys Tyr Asp Asn His Leu Gln Gln Phe Asn Ser Phe His Asn Asn Pro
226      740                745                750
228 Thr His Glu Ser Asn Ser Leu Pro Pro Ser Pro Leu Arg Ile Val Glu
229           755                760                765
231 Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala Gln Glu Pro
232      770                775                780
234 Pro Lys Lys Leu Thr Asn Ser Arg Arg Val Lys Arg Thr Lys Pro Asn
235 785           790                795                800
237 Gly His Ile Ser Ser Arg Val Glu Val Asp Ser Asp Thr Ser Ser Gln
238           805                810                815
240 Ser Thr Ser Ser Glu Ser Glu Thr Glu Asp Glu Arg Ile Gly Glu Asp
241      820                825                830
243 Thr Pro Phe Leu Ser Ile Gln Asn Pro Met Ala Thr Ser Leu Glu Pro
244      835                840                845
246 Ala Ala Ala Tyr Arg Leu Ala Glu Asn Arg Thr Asn Pro Ala Asn Arg
247      850                855                860
249 Phe Ser Thr Pro Glu Glu Leu Gln Ala Arg Leu Ser Ser Val Ile Ala
250 865           870                875                880
W--> 252 Asn Gln Asp Pro Ile Ala Val (Xaa) Asp Ile Asn Lys Thr His Arg Phe
253           885                890                895
255 Thr Cys Lys Thr Leu Phe Tyr Ile Met Lys Tyr Ser Thr Phe Lys Leu
256           900                905                910
258 Asn Asn Leu Phe Tyr Phe Ser Asn Ser Ala Asp Arg Lys Gln Glu Trp
259      915                920                925
W--> 261 Lys Lys Lys Leu Leu (Xaa) Ile Lys Tyr Thr Tyr Val Gln Met Cys Tyr
262      930                935                940
264 Val Pro Tyr Val Ala Ile Phe Tyr Ser Ile Ser Lys Met Gly Lys Asp
265 945           950                955                960
```

refer to p. 2

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            RAW SEQUENCE LISTING                  DATE: 11/20/2000
            PATENT APPLICATION:  US/09/312,596    TIME: 08:38:38

            Input Set : A:\593601.app
            Output Set: N:\CRF3\11202000\I312596.raw
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```
      267 Ile Asn Gly Ala Phe Met Leu Cys Tyr Val Glu Ser Lys Phe Cys Thr
      268            965                    970                    975
W-->  270 Ala Thr Met Ile Ala Val Pro (Xaa) Tyr Phe Ala Lys Pro Ser Ser Pro
      271            980                   985                    990
      273 Gln Leu Phe Trp Leu Phe Cys Ala Leu His Tyr Asn Asp Trp Met Tyr
      274            995                   1000                   1005
      276 Asp Leu Gln Glu Gln Lys Ser Pro Phe Ala Cys Cys Gly Ile Pro
      277       1010                  1015                  1020
      279 Arg Ser Lys Ser Pro Val Met Ala Leu Thr Pro Tyr Pro Leu His Gln
      280 1025                  1030                  1035                  1040
      282 Glu Lys Lys Lys Ile Lys Lys Lys Lys Lys Lys Arg Lys Gln Arg
      283            1045                  1050                  1055
W-->  285 Glu Lys Arg Lys Glu Lys Glu Lys Lys Ser (Xaa) Lys Asn Lys
      286            1060                  1065                  1070
      289 <210> SEQ ID NO: 3
      290 <211> LENGTH: 1351
      291 <212> TYPE: DNA
      292 <213> ORGANISM: HUMAN DARTA
      294 <400> SEQUENCE: 3
      295 cggcctataa gatgctgtat catttggttg gggggggcctc tgcgtggtaa tggaccgtaa   60
      296 gacaggccag gccttcttct ggaggtgagc cgatggagat ttattcccca gacatgtcta  120
      297 aggtcgccag cgagaggtcc tccagcccct ccactcagct gagtgcagac ccatctcttg  180
      298 atgggcttcc ggcagcagaa gacatgccag agcccagac tgaagatggg aggaaccctg   240
      299 gactcgtggg cctggccgtg ccctgctgtg cgtgcctaga agctgagcgc ctgagaggtt  300
      300 gcctcaactc agagaaaatc tgcattgtcc ccatcctgac ttgcctggtc agcctctgcc  360
      301 tctgcatcgc cggcctcaag tgggtatttg tggacaagat cttttgaatat gactctccta  420
      302 ctcacctta ccctggggag taggccagg acccatatat ttctctggac gcaactgctg   480
      303 cctcagctgt gtgggtgtcg tctgaggcat acacttcacc tgtctctagg gctcaatcta  540
      304 aaagtgaggt tcaagttaca gtgcaaggtg acaaggctgt tgtctccttt gaaccatcag  600
      305 cggcaccgac accgaagaat cgtattttg ccttttcttt ctgccgtcc actgcgccat   660
      306 ccttccttc acccacccgg aaccctgagg tgagaacgcc caagtcagca actcaaccac  720
      307 aacaacaga aactaatctc caaactgctc ctaaactttc tacatctaca tccaccactg  780
      308 ggacaagcca tcttttaaaa tgtgcggaga aggagaaaac tttctgtatg aatggagggg  840
      309 agtgcttcat ggttaaagac cttcaaacc cctcgagata cttgtgcaaa ggcggaggag   900
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      311 atcatgtgtg tggtggccta ctgcaaaacc aagaaacagc gggaaaaagct gcatgaccgt 1020
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      314 atctccagtg agcatattgt tgagagagaa gcagagacat ccttttccac cagtcactat 1200
      315 acttccacag cccatcactc cactactgtc acccagactc ctagccacag ctggagcaac 1260
      316 ggacacactg aaagcatcct ttccgaaagc cactctgtaa tcgtgatgtc atccgtagaa 1320
      317 aacagtaggc acagcagccc aactggggcc g                                1351
      320 <210> SEQ ID NO: 4
      321 <211> LENGTH: 448
      322 <212> TYPE: PRT
      323 <213> ORGANISM: HUMAN DARTA
      325 <100> SEQUENCE: 4
W-->  326 Ala Cys Lys Met Leu Tyr His Leu Val Gly Gly Ala Ser Ala Trp (Xaa)
      327   1                 5                 10                15
```

(handwritten annotations) refer to p. 2.

same refer to p. 2 please check all of sequence #4 for "Xaa's".

VERIFICATION SUMMARY   DATE: 11/20/2000
PATENT APPLICATION: US/09/312,596   TIME: 08:38:39

  Input Set : A:\593601.app
  Output Set: N:\CRF3\11202000\I312596.raw

```
L:90 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:90 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:90 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:90 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:90 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:93 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:93 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:93 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:93 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
M:340 Repeated in SeqNo:2
L:108 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:108 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:108 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:108 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:117 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:117 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:117 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:117 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:120 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:120 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:120 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:120 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:123 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:123 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:123 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:123 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:252 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:252 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:252 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:252 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:261 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:261 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:261 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:261 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:270 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:270 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:270 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:285 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:285 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:285 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:285 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:326 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:326 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:326 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:326 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:326 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:389 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/312,596

DATE: 11/20/2000
TIME: 08:38:39

Input Set : A:\593601.app
Output Set: N:\CRF3\11202000\I312596.raw

```
L:389 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:389 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:389 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
M:340 Repeated in SeqNo 4
L:392 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:392 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
```